



RAW SEQUENCE LISTING ERROR REPORT

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Application Serial Number: 09/955,737
Source: FW/b
Date Processed by STIC: 8/6/04

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- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
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<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

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Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box-1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
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Revised 05/17/04



IFW16

RAW SEQUENCE LISTING

DATE: 08/06/2004

PATENT APPLICATION: US/09/955,737

TIME: 10:54:14

Input Set : A:\16163-015001.TXT

Output Set: N:\CRF4\08062004\I955737.raw

Does Not Comply
Corrected Diskette Needed

4 <110> APPLICANT: Chopra , Rajiv
 5 Svenson, Kristine
 6 Annis, Bethany
 7 Akopian, Tatos N.
 8 Bard, Jonathan A.
 9 Stahl, Mark L.
 10 Somers, William Stuart
 13 <120> TITLE OF INVENTION: CRYSTAL STRUCTURE OF BACE AND USES
 14 THEREOF
 16 <130> FILE REFERENCE: 16163-015001
 18 <140> CURRENT APPLICATION NUMBER: US 09/955,737
 19 <141> CURRENT FILING DATE: 2001-09-19
 21 <150> PRIOR APPLICATION NUMBER: US 60/234,576
 22 <151> PRIOR FILING DATE: 2000-09-22
 24 <160> NUMBER OF SEQ ID NOS: 6
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 28 <210> SEQ ID NO: 1
 29 <211> LENGTH: 501
 30 <212> TYPE: PRT
 31 <213> ORGANISM: Homo sapiens
 33 <400> SEQUENCE: 1
 34 Met Ala Gln Ala Leu Pro Trp Leu Leu Leu Trp Met Gly Ala Gly Val
 35 1 5 10 15
 36 Leu Pro Ala His Gly Thr Gln His Gly Ile Arg Leu Pro Leu Arg Ser
 37 20 25 30
 38 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp
 39 35 40 45
 40 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val
 41 50 55 60
 42 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr
 43 65 70 75 80
 44 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser
 45 85 90 95
 46 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr
 47 100 105 110
 48 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val
 49 115 120 125
 50 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp
 51 130 135 140
 52 Leu Val Ser Ile Pro His Gly Pro Asn Val Thr Val Arg Ala Asn Ile
 53 145 150 155 160
 54 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp
 55 165 170 175

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56 Glu Gly Ile Leu Gly Leu Ala Tyr Ala Glu Ile Ala Arg Pro Asp Asp
57          180          185          190
58 Ser Leu Glu Pro Phe Phe Asp Ser Leu Val Lys Gln Thr His Val Pro
59          195          200          205
60 Asn Leu Phe Ser Leu Gln Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln
61          210          215          220
62 Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile
63 225          230          235          240
64 Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg
65          245          250          255
66 Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln
67          260          265          270
68 Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val
69          275          280          285
70 Asp Ser Gly Thr Thr Asn Leu Arg Leu Pro Lys Lys Val Phe Glu Ala
71          290          295          300
72 Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp
73 305          310          315          320
74 Gly Phe Trp Leu Gly Glu Gln Leu Val Cys Trp Gln Ala Gly Thr Thr
75          325          330          335
76 Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val
77          340          345          350
78 Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg
79          355          360          365
80 Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala
81          370          375          380
82 Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu
83 385          390          395          400
84 Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala
85          405          410          415
86 Val Ser Ala Cys His Val His Asp Glu Phe Arg Thr Ala Ala Val Glu
87          420          425          430
88 Gly Pro Phe Val Thr Leu Asp Met Glu Asp Cys Gly Tyr Asn Ile Pro
89          435          440          445
90 Gln Thr Asp Glu Ser Thr Leu Met Thr Ile Ala Tyr Val Met Ala Ala
91          450          455          460
92 Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp
93 465          470          475          480
94 Arg Cys Leu Arg Cys Leu Arg Gln Gln His Asp Asp Phe Ala Asp Asp
95          485          490          495
96 Ile Ser Leu Leu Lys
97          500
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 695
101 <212> TYPE: PRT
102 <213> ORGANISM: Homo sapiens
104 <400> SEQUENCE: 2
105 Met Leu Pro Gly Leu Ala Leu Leu Leu Leu Ala Ala Trp Thr Val Trp
106 1          5          10          15

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```

107 Ala Leu Glu Val Pro Thr Asp Gly Asn Ala Gly Leu Leu Ala Glu Pro
108      20      25      30
109 Gln Ile Ala Met Phe Cys Gly Arg Leu Asn Met His Met Asn Val Gln
110      35      40      45
111 Asn Gly Lys Trp Asp Ser Asp Pro Ser Gly Thr Lys Thr Cys Ile Asp
112      50      55      60
113 Thr Lys Glu Gly Ile Leu Gln Tyr Cys Gln Glu Val Tyr Pro Glu Leu
114 65      70      75      80
115 Gln Ile Thr Asn Val Val Glu Ala Asn Gln Pro Val Thr Ile Gln Asn
116      85      90      95
117 Trp Cys Lys Arg Gly Arg Lys Gln Cys Lys Thr His Pro His Phe Val
118      100     105     110
119 Ile Pro Tyr Arg Cys Leu Val Gly Glu Phe Val Ser Asp Ala Leu Leu
120      115     120     125
121 Val Pro Asp Lys Cys Lys Phe Leu His Gln Glu Arg Met Asp Val Cys
122      130     135     140
123 Glu Thr His Leu His Trp His Thr Val Ala Lys Glu Thr Cys Ser Glu
124 145     150     155     160
125 Lys Ser Thr Asn Leu His Asp Tyr Gly Met Leu Leu Pro Cys Gly Ile
126      165     170     175
127 Asp Lys Phe Arg Gly Val Glu Phe Val Cys Cys Pro Leu Ala Glu Glu
128      180     185     190
129 Ser Asp Asn Val Asp Ser Ala Asp Ala Glu Glu Asp Asp Ser Asp Val
130      195     200     205
131 Trp Trp Gly Gly Ala Asp Thr Asp Tyr Ala Asp Gly Ser Glu Asp Lys
132      210     215     220
133 Val Val Glu Val Ala Glu Glu Glu Val Ala Glu Val Glu Glu Glu
134 225     230     235     240
135 Glu Ala Asp Asp Asp Glu Asp Asp Glu Asp Gly Asp Glu Val Glu Glu
136      245     250     255
137 Glu Ala Glu Glu Pro Tyr Glu Glu Ala Thr Glu Arg Thr Thr Ser Ile
138      260     265     270
139 Ala Thr Thr Thr Thr Thr Thr Thr Glu Ser Val Glu Glu Val Val Arg
140      275     280     285
141 Val Pro Thr Thr Ala Ala Ser Thr Pro Asp Ala Val Asp Lys Tyr Leu
142      290     295     300
143 Glu Thr Pro Gly Asp Glu Asn Glu His Ala His Phe Gln Lys Ala Lys
144 305     310     315     320
145 Glu Arg Leu Glu Ala Lys His Arg Glu Arg Met Ser Gln Val Met Arg
146      325     330     335
147 Glu Trp Glu Glu Ala Glu Arg Gln Ala Lys Asn Leu Pro Lys Ala Asp
148      340     345     350
149 Lys Lys Ala Val Ile Gln His Phe Gln Glu Lys Val Glu Ser Leu Glu
150      355     360     365
151 Gln Glu Ala Ala Asn Glu Arg Gln Gln Leu Val Glu Thr His Met Ala
152      370     375     380
153 Arg Val Glu Ala Met Leu Asn Asp Arg Arg Arg Leu Ala Leu Glu Asn
154 385     390     395     400
155 Tyr Ile Thr Ala Leu Gln Ala Val Pro Pro Arg Pro Arg His Val Phe

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```

156          405          410          415
157 Asn Met Leu Lys Lys Tyr Val Arg Ala Glu Gln Lys Asp Arg Gln His
158          420          425          430
159 Thr Leu Lys His Phe Glu His Val Arg Met Val Asp Pro Lys Lys Ala
160          435          440          445
161 Ala Gln Ile Arg Ser Gln Val Met Thr His Leu Arg Val Ile Tyr Glu
162          450          455          460
163 Arg Met Asn Gln Ser Leu Ser Leu Leu Tyr Asn Val Pro Ala Val Ala
164 465          470          475          480
165 Glu Glu Ile Gln Asp Glu Val Asp Glu Leu Leu Gln Lys Glu Gln Asn
166          485          490          495
167 Tyr Ser Asp Asp Val Leu Ala Asn Met Ile Ser Glu Pro Arg Ile Ser
168          500          505          510
169 Tyr Gly Asn Asp Ala Leu Met Pro Ser Leu Thr Glu Thr Lys Thr Thr
170          515          520          525
171 Val Glu Leu Leu Pro Val Asn Gly Glu Phe Ser Leu Asp Asp Leu Gln
172          530          535          540
173 Pro Trp His Ser Phe Gly Ala Asp Ser Val Pro Ala Asn Thr Glu Asn
174 545          550          555          560
175 Glu Val Glu Pro Val Asp Ala Arg Pro Ala Ala Asp Arg Gly Leu Thr
176          565          570          575
177 Thr Arg Pro Gly Ser Gly Leu Thr Asn Ile Lys Thr Glu Glu Ile Ser
178          580          585          590
179 Glu Val Lys Met Asp Ala Glu Phe Arg His Asp Ser Gly Tyr Glu Val
180          595          600          605
181 His His Gln Lys Leu Val Phe Phe Ala Glu Asp Val Gly Ser Asn Lys
182          610          615          620
183 Gly Ala Ile Ile Gly Leu Met Val Gly Gly Val Val Ile Ala Thr Val
184 625          630          635          640
185 Ile Val Ile Thr Leu Val Met Leu Lys Lys Lys Gln Tyr Thr Ser Ile
186          645          650          655
187 His His Gly Val Val Glu Val Asp Ala Ala Val Thr Pro Glu Glu Arg
188          660          665          670
189 His Leu Ser Lys Met Gln Gln Asn Gly Tyr Glu Asn Pro Thr Tyr Lys
190          675          680          685
191 Phe Phe Glu Gln Met Gln Asn
192          690          695

```

194 <210> SEQ ID NO: 3

195 <211> LENGTH: 9

196 <212> TYPE: PRT

197 <213> ORGANISM: Artificial Sequence

199 <220> FEATURE:

200 <223> OTHER INFORMATION: APP inhibitor peptide

W--> 202 <221> NAME/KEY: VARIANT

203 <222> LOCATION: 5

204 <223> OTHER INFORMATION: Xaa = Sta = Statine

W--> 206 <400> 3

W--> 207 Ser Glu Val Asn Xaa Val Ala Glu Phe

208 1 5

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Input Set : A:\16163-015001.TXT

Output Set: N:\CRF4\08062004\I955737.raw

210 <210> SEQ ID NO: 4
 211 <211> LENGTH: 29
 212 <212> TYPE: DNA
 213 <213> ORGANISM: Artificial Sequence
 215 <220> FEATURE:
 216 <223> OTHER INFORMATION: Primer
 218 <400> SEQUENCE: 4
 219 gctctagaac ccagcacggc atccggctg 29
 221 <210> SEQ ID NO: 5
 222 <211> LENGTH: 42
 223 <212> TYPE: DNA
 224 <213> ORGANISM: Artificial Sequence
 226 <220> FEATURE:
 227 <223> OTHER INFORMATION: Primer
 229 <400> SEQUENCE: 5
 230 ccaagcatgc ggccgcaata ggctatggtc atgaggggtg ac 42
 232 <210> SEQ ID NO: 6
 233 <211> LENGTH: 12
 234 <212> TYPE: PRT
 235 <213> ORGANISM: Artificial Sequence
 237 <220> FEATURE:
 238 <223> OTHER INFORMATION: Synthetically generated peptide
 W--> 240 <221> NAME/KEY: VARIANT
 241 <222> LOCATION: 1
 242 <223> OTHER INFORMATION: Xaa = Abz = amino benzoic acid
 W--> 244 <221> VARIANT
 245 <222> LOCATION: 12
 246 <223> OTHER INFORMATION: Xaa = = Dpa = 9,10-diphenylanthracene
 W--> 248 <400> 6
 W--> 249 Xaa Ser Glu Val Asn Leu Asp Ala Glu Phe Arg Xaa
 250 1 5 10

FYI: Xaa can only
 represent a
 single amino
 acid
 nothing else

RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:3; Xaa Pos. 5

Seq#:6; Xaa Pos. 1,12

VERIFICATION SUMMARY

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Input Set : A:\16163-015001.TXT

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L:202 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:206 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:0
L:240 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:244 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:248 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:6
L:249 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0